Basic approaches to gene expression analysis of stem cells by microarrays.

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Public Summary:

In this report we focus on the state-of-the-art analysis of microarray data and introduce the reader to important controls that yield robust biologically relevant results.

Scientific Abstract:

This chapter covers gene expression analysis by microarray to study and characterize stem cells. In a case-study scenario, we describe basic bioinformatic methodologies used to answer common questions in microarray experiments involving one or more stem cell populations. Service providers or departmental core labs usually carry out sample preparation, hybridization, and scanning of microarrays. Therefore, in this chapter, we focus on the state-of-the-art data analysis that avoids common pitfalls and introduces the reader to important controls that yield robust biologically relevant results. We describe evaluation of differentially expressed genes, clustering methods, gene-set enrichment analysis, and gene network discovery methods that can be used to formulate meaningful biological insights as well as suggest new wet lab experiments.

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